

[illegible]

[illegible][illegible]

to the right is RP11-150013, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-150016; actual end is at 46953 of RP11-150013.

FEATURES

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repeat_region
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repeat_region
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repeat_region

REVIEWER: Home sapiens.
AUTHOR: Home sapiens
REMARKS: Rikuyoshi, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1. Bases 1 to 147903
Submitted (J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
9064792
MELLINE
3847874
2. Bases 1 to 147903
Submitted (Kohlfelt, T., Maupin, R., Hawkins, M. and Davidson, T.
The sequence of Homo sapiens BAC clone RP11-150016
Unpublished
3. Bases 1 to 147903
Submitted (Waterston, R.H.
Direct Submission
Submitted (29-MAY-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4. Bases 1 to 147903
Submitted (Waterston, R.H.
Direct Submission
Submitted (08-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5. Bases 1 to 147903
Submitted (Waterston, R.
Direct Submission
Submitted (10-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Sep 9, 1999 this sequence version replaced at 5101898.
Center: Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@wustl.edu
Summary Statistics
Center project name: H_NH0355F16
NOTE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 40); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis, Mo. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>
SOURCE INFORMATION:
The RP11-150016 BAC library was made from the blood of one male donor, as described by Osoegawa, K., Watanabe, Y., Shimizu, E., Tatematsu, M., Catanesi, J.C., and de Jong, P.J. (1994) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5:11-18. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pierre de Jong and coworkers at the Biomedical Research Institute (<http://biomed.med.buffalo.edu>)
VECTOR: pBAC3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-1319A7; the clone sequenced

[illegible]


```

XX ABK11.9;
XX
XX 16 JUN 2002 (first entry)
XX
XX Human DNA representing the Tachykinin Receptor 1, TACR1, gene.
XX
XX Human, de. gene, TACR1, Tachykinin Receptor 1, chromosome 2;
XX SNR, single nucleotide polymorphism, gene therapy; haplotype; genotype;
XX pain; depression; vomiting; acute inflammatory diarrhoea;
XX opiate addiction; drug screening.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
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XX /label= SNR
XX /note= "Single nucleotide polymorphism"
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XX /tag= b
XX /label= SNP
XX /note= "Single nucleotide polymorphism"
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XX WO200216399 A2.
XX
XX 28 FEB 2002.
XX
XX 27 AUG 2001; 2001WO 080666A.
XX
XX 25-AUG-2000; 2000US-227815P.
XX (CFNA-) GENAISSANCE PHARM INC.
XX
XX Anastasio AE, Kazemi A;
XX
XX WPI; 2002-280907/32.
XX P-PSDB; AAU7B238.
XX
XX Novel isolated polymorphisms which is a polymorphic variant of
XX tachykinin receptor 1 (TACR1) gene useful for exploring TACR1 protein
XX isoform used in screening drug candidates to treat pain, depression,
XX vomiting
XX
XX Claim 1; Fig 1; 80pp; English.
XX
XX The invention relates to an isolated polymorphic site sequence which
XX comprises a tachykinin receptor 1 (TACR1) isoform (30) that is any one of
XX 16 CC as given in specification, where each CC comprises specific regions
XX of the TACR1 genomic DNA appearing as ABK11.9, and is defined by
XX polymorphism positions (p1) 3164, 3319, 3906, 4339, 4444, 4491b,
XX 94601, 94821, 94960, 94960. Also included are fragments of the
XX TACR1 sequence and TACR1 cDNA, a transgenic non-human animal transformed
XX with the TACR1 sequence or coding region, haplotyping (or genotyping) the
XX TACR1 of an individual by determining either the haplotype of one or both
XX copies of the TACR1 gene, predicting the haplotype pair for the
XX TACR1 gene of an individual, identifying an association between a trait
XX and a haplotype pair, an isolated oligonucleotide for detecting the
XX polymorphisms, a computer system for storing and analyzing polymorphism
XX data and a genome anthology for TACR1 gene. The TACR1 isoform is useful
XX for studying expression and function of TACR1 and expressing TACR1
XX protein for use in screening for candidate drugs to treat diseases
XX related to TACR1 activity. The polymorphism and haplotype data is useful
XX for validating whether TACR1 is a suitable target for drugs to treat
XX pain, depression, vomiting, acute inflammatory diarrhoea and opiate
XX addiction, screening for such drugs and reducing bias in clinical trials
XX of such drugs. The genotyping method is useful for determining whether an
XX individual has one of the haplotype pairs. The haplotyping method is
XX useful for improving efficiency and outcome of several steps in
XX discovery and development of drugs for treating the diseases. The
XX haplotyping method is also useful for validating TACR1 as a candidate
XX target for treating a specific condition or disease predicted to be
XX associated with TACR1 activity. The method is also useful for screening
XX compounds to treat a specific condition or disease predicted to be
XX associated with TACR1 activity. The methods are useful for identifying
XX an association between susceptibility to a disease, or being of a disease,
XX or response to a drug. The gene for TACR1 is located on human
XX chromosome 2. The present sequence is a representative gene sequence
XX for TACR1.
XX
XX Sequence 94690 BP; 24293 A; 26385 C; 20052 G; 28885 T; 76 others;
XX
XX Query Match 11.6%; Score 203; DB 24; Length 94690;
XX Best Local Similarity 29.2%; Read: 94690; 48;

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Matches 256; Conservative 0; Mismatches 61; Indels 14; Gaps 2;
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 T 1414 TAAAGATTTTGAAGAGTGTGGTAAAGTGGTCAATGCTGTAAATGCTCAAGAGTTGGAG 2383
 TT
 Y 1469 TTTTATTTTGAAGAGTGTGGTAAAGTGGTCAATGCTGTAAATGCTCAAGAGTTGGAG 2443
 TT
 DB 1494 TTTTATTTTGAAGAGTGTGGTAAAGTGGTCAATGCTGTAAATGCTCAAGAGTTGGAG 2443
 TT
 Y 1500 AACGTCATTTTAAAGAGTGTGGTAAAGTGGTCAATGCTGTAAATGCTCAAGAGTTGGAG 1588
 TT
 DB 2444 AACGTCATTTTAAAGAGTGTGGTAAAGTGGTCAATGCTGTAAATGCTCAAGAGTTGGAG 2503
 TT
 Y 1529 CATGTCATTTTAAAGAGTGTGGTAAAGTGGTCAATGCTGTAAATGCTCAAGAGTTGGAG 1648
 TT
 DB 2504 CATGTCATTTTAAAGAGTGTGGTAAAGTGGTCAATGCTGTAAATGCTCAAGAGTTGGAG 2551
 TT
 Y 1649 AAGGTCATTTTAAAGAGTGTGGTAAAGTGGTCAATGCTGTAAATGCTCAAGAGTTGGAG 1708
 TT
 DB 2562 AAGGTCATTTTAAAGAGTGTGGTAAAGTGGTCAATGCTGTAAATGCTCAAGAGTTGGAG 2609
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 Y 1729 ACTGTCATTTTAAAGAGTGTGGTAAAGTGGTCAATGCTGTAAATGCTCAAGAGTTGGAG 1739
 TT
 DB 2610 ACTGTCATTTTAAAGAGTGTGGTAAAGTGGTCAATGCTGTAAATGCTCAAGAGTTGGAG 2640
 TT
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 ID AAA80253 standard; DNA; 72928 BP.
 XX
 AC AAA80253;
 XX
 DT 22 NOV 2000 (first entry)
 XX
 DE Human ASTH1J 5' genomic region.
 XX
 KW ASTH1J locus; human; chromosome 11p; asthma;
 KW bronchial hyperactivity; etc family; transcription factor;
 KW splice variants; genetic predispositions; polymorphism; antibody;
 KW drug screening; prophylaxis; therapy; diagnostics; dr.
 XX
 OS Homo sapiens.
 XX
 PN US6087485-A.
 XX
 PD 11-JUL-2000.
 XX
 PF 21-JAN-1998; 98US 0009913.
 XX
 PR 21-JAN-1997; 97US 0035663.
 PR 01-JUL-1997; 97US 0051432.
 XX
 RA (AASYS) AXYS PHARM INC.
 XX
 PI Calvin M, Miller A, North M, Cardon L, Buckler A;
 PI Brooks Wilson AP, Carey AH;
 PI WPI; 2000-06169/45.
 XX
 PT New nucleic acids other than naturally occurring chromosomes encoding
 PT ASTH1 protein, for e.g. screening compositions that modulate expression
 PT or function of Asth1 proteins or as diagnostics for genetic
 PT predisposition to asthma
 XX
 DS Claim 7; Column 49-112; 14pp; English.

CC therapeutic. The present sequence represents a human ASTH1 genomic region
 CC sequence.
 XX
 SQ Sequence 72928 BP; 20042 A; 15100 C; 16036 G; 21750 T; 0 other;
 Query Match 10.6%; Score 185.2; DB 20; Length 72928;
 Post-Local Similarity 41.7%; Prod No. 8.4e 44;
 Matches 255; Conservative 0; Mismatches 43; Indels 14; Gaps 2;
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 TT
 DB 38946 GTTCAGTGGTGTGGTGTAAATGCTGTAAATGCTCAAGAGTTGGAGTGTAAATGCTCAAGAGTTGGAG 48847
 TT
 Y 1489 TGAGTCAGTGGTGTAAATGCTGTAAATGCTCAAGAGTTGGAGTGTAAATGCTCAAGAGTTGGAG 1547
 TT
 DB 38886 TGAGTCAGTGGTGTAAATGCTGTAAATGCTCAAGAGTTGGAGTGTAAATGCTCAAGAGTTGGAG 16627
 TT
 Y 1548 TACACATTAATGCTGTAAATGCTGTAAATGCTCAAGAGTTGGAGTGTAAATGCTCAAGAGTTGGAG 1607
 TT
 DB 38826 TATAAACTTACCCAGTGTAAATGCTGTAAATGCTCAAGAGTTGGAGTGTAAATGCTCAAGAGTTGGAG 38779
 TT
 Y 1608 TTGGAGGCTGTAAATGCTGTAAATGCTCAAGAGTTGGAGTGTAAATGCTCAAGAGTTGGAGTGTAAATGCTCAAGAGTTGGAG 1667
 TT
 DB 38778 TTGGAGGCTGTAAATGCTGTAAATGCTCAAGAGTTGGAGTGTAAATGCTCAAGAGTTGGAGTGTAAATGCTCAAGAGTTGGAG 16719
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 Y 1668 GATTGTCATTTGCTGTAAATGCTGTAAATGCTCAAGAGTTGGAGTGTAAATGCTCAAGAGTTGGAG 1727
 TT
 DB 38718 GATTGTCATTTGCTGTAAATGCTGTAAATGCTCAAGAGTTGGAGTGTAAATGCTCAAGAGTTGGAG 38660
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 Y 1728 AAAAAAAAAAAAAA 1739
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 DB 38659 AAAAAAAAAAAAAA 38648

RESULT 7
 AAA80253/c
 ID AAA80253 standard; DNA; 72928 BP.
 XX
 AC AAA80253;
 XX
 DT 22 NOV 2000 (first entry)
 XX
 DE Human ASTH1J 5' genomic region.
 XX
 KW ASTH1J locus; human; chromosome 11p; asthma;
 KW bronchial hyperactivity; etc family; transcription factor;
 KW splice variants; genetic predispositions; polymorphism; antibody;
 KW drug screening; prophylaxis; therapy; diagnostics; dr.
 XX
 OS Homo sapiens.
 XX
 PN US6087485-A.
 XX
 PD 11-JUL-2000.
 XX
 PF 21-JAN-1998; 98US 0009913.
 XX
 PR 21-JAN-1997; 97US 0035663.
 PR 01-JUL-1997; 97US 0051432.
 XX
 RA (AASYS) AXYS PHARM INC.
 XX
 PI Calvin M, Miller A, North M, Cardon L, Buckler A;
 PI Brooks Wilson AP, Carey AH;
 PI WPI; 2000-06169/45.
 XX
 PT New nucleic acids other than naturally occurring chromosomes encoding
 PT ASTH1 protein, for e.g. screening compositions that modulate expression
 PT or function of Asth1 proteins or as diagnostics for genetic
 PT predisposition to asthma
 XX
 DS Claim 7; Column 49-112; 14pp; English.


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NAME/KEY: allele
LOCATION: 88040...88096
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NAME/KEY: allele
LOCATION: 88050...88096
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FEATURE:
NAME/KEY: allele
LOCATION: 90819...90865
OTHER INFORMATION: complement polymorphic fragment 90-143-254
FEATURE:
NAME/KEY: allele
LOCATION: 91690...91746
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NAME/KEY: allele
LOCATION: 92699...92747
OTHER INFORMATION: polymorphic fragment 5-128-66 SEQ ID63
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LOCATION: 97099...97145
OTHER INFORMATION: polymorphic fragment 99-144-224 SEQ ID33
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LOCATION: 97746...97797
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
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NAME/KEY: allele
LOCATION: 98094...98131
OTHER INFORMATION: polymorphic fragment 5-130-267 SEQ ID65
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LOCATION: 98094...99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
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Best Local Similarity 75.58;  Pred. No. 2,76+42;
Matches 246;  Conservat. 0;  Mismatches 66;  Indels 14;  Gaps 0

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DB  129555  AAATCTCTATGCTGCTGAGGCTAGAGGCTAAAGCTCTGAAACCTGAGCTGCTGCAATATATGCAAAAGCTG 129496

QY  1473  AGCCGCGAGATGCTGTTGAGGTTCAGAGCTTTGAAACAGCTGCTGCAATATATGCAAAAGCTG 1512
DB  129495  AGCTGCAAGATGATCATCTGAGCTTCAGAGCTTCAGACAGCTGCTGCAATATATGCAAAAGCTG 129486

QY  1533  CCATTCTATATATAATACAGAAATTTAGCCAGAGTGTGGTGGTCTGATGCTGTAATATGTAATGATG 1592
DB  129436  CAGTCTCTACAAAAACAAAAAATTAGCCAGAGCTCATGAGGCTGATGAGGCTGATGCTGATGCTGTA 129479

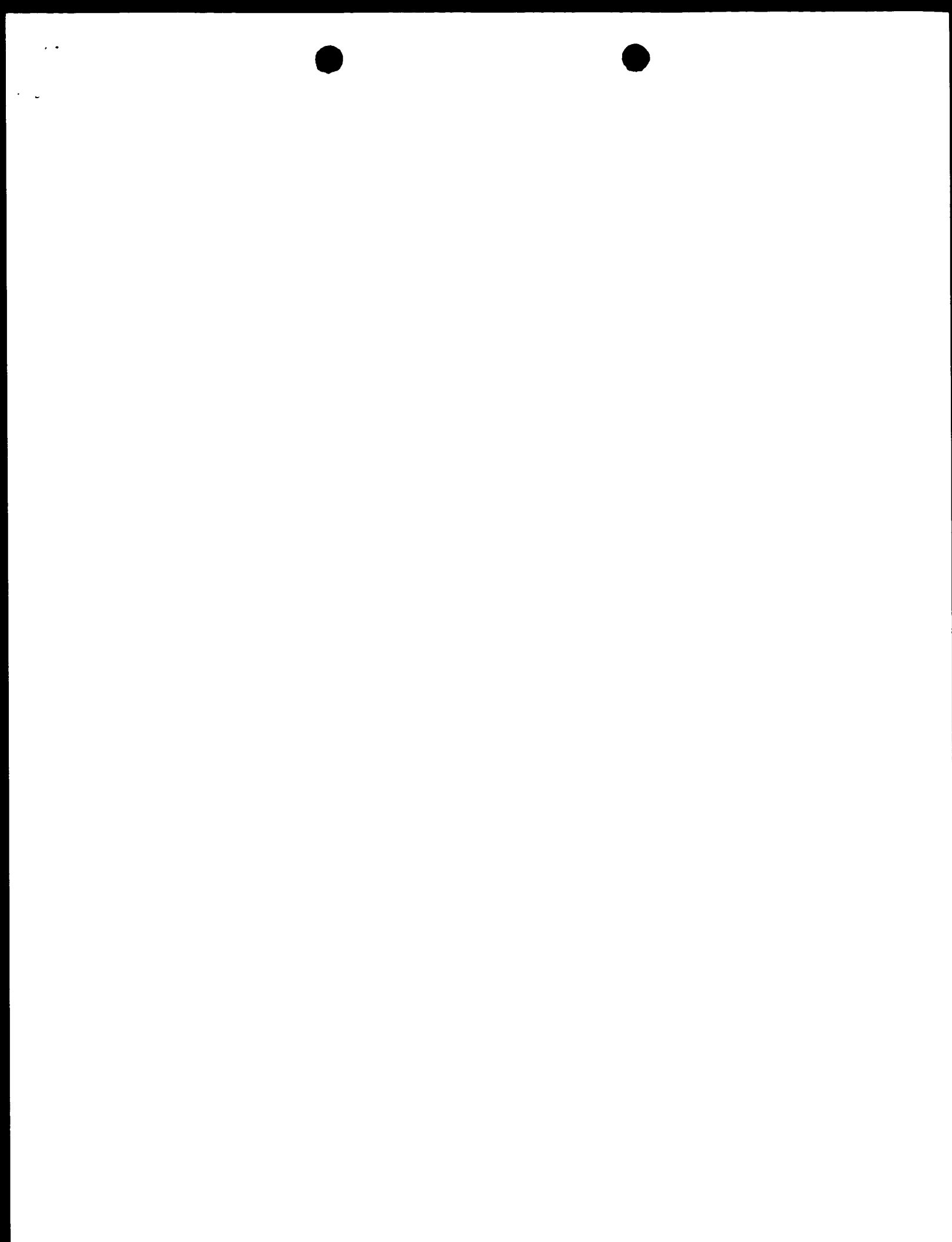
QY  1593  CCTGTAAATCCAGCTCTGGAGAGCTTGAGGCAAGAGAAATCATTTAAATCCATAGAGTGAAG 1652
DB  129377  -----GCTATCTGGAGAGAGCTGAGGATGAGAAATGAGCTGTAATCCATAGAGTGAAG 129348

QY  1653  GTTGAGTGAATGAGATTTGAGTGAAGCTATGCTCATCTCCAGCTGCTGCTGCTGCTGCTGCTGCTG 1712
DB  129327  GTTGAGTGAATGAGTGAAGTGAATGCTCATCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129276

QY  1713  CTTGTCGTGAAAAAAMAAAAAAMAAAAA 1718
DB  129069  GAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 129044

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Query Match	9.9%	Score 172.6	DB 4	Length 36139
Best Local Similarity	78.0%	Pred. No. 1.30 42		



[illegible][illegible]

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ORIGIN	/nc6.wvart: gpal:EGAT: 2.14.1 EGAT: 2.14.3 EGAT:				
	Caltech Human PAC Library Dn				

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Best Local Contig	100	2317
Matches	100	2317

[illegible][illegible][illegible]

Table 1. *Continued*

[illegible]

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P0000
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sequence.	
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VERSION	01.010.740
NUMBERS	000

[illegible]

ATTACHED TO THE FOLLOWING TITLE
Use of a PAC End-Spin Catheter for Collecting Body Wt.
Data - Abstract 110001

Contact: Mark Adams
Department of Ecology and
The Institute for Genomic Research

Tel : 33 1 43 00 00
Fax : 33 1 43 00 00
Email : mda@msi.fr

end search page:
http://www.1st-23.com/4/kingdom/4-01_search/4-01_search.html
Seq primer: T7

FEATURES	LOCATION/Qualifiers
SOURCE	1. 379
	/organism "Homo sapiens"

[illegible]

Caltech Human BAC Library A^u

FILE NUMBER	DATE	BY	PAGE	OTHERS
ORIGIN				

Category	Score	Weight	Weighted Score
Best Local Similarity	70.79	1.00	70.79
Weighted Average	69.26	1.00	69.26
Best Local Similarity	70.79	1.00	70.79
Weighted Average	69.26	1.00	69.26

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LOCUS AA084439
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EST c12777

AA084439	element, RNA sequence.
ACCESSION	AA084439
VERSION	GI-1626693

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HILLER, L. EMMETT, J. E. FORT, J. E., SCHW, W., HAWKINS

E. Morris, M. Edwards, C. Langdon, S. Evans, J. Ewing, T. Schellens, R. Bates, M. Alf, A. Wajsb, I. Kovacs, F. Underwood, K. Wohlmann, D. Waterson, P. Wilson, P. and Maria, M.

[illegible]

444 E. 10th St. E. S. 5501, C. 1000, M. 63109
Tel: 314 236 1800
Fax: 314 396 1810

This service is available again free through the IMAGE Consortium (<http://image.lim.gov>) for further information. Seq primer: -40M13 fwd. from Amersham High quality sequenced strand.

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/lab host="SGER (kanamycin resistant)"
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XhoI: cloned unidirectionally. Primer: Oligo dT. N12
(Ntera-2/cl.01) precursor cells induced with Retinoic
Acid for 1 week, followed by 3 weeks in mitotic inhibitors
(RepRap #2). Average insert size: 1.1 kb; Uni-ZAP XP
Vector; -5' adaptor sequence: 5' GAATTCAGACAG 3' -3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'
RAMP COUNT 111 a 129 c 80 g 139 t 2 others
REPIN
Query March 10.48; Score 181.4; DB 9; Length 461;
Best local Similarity 79.15; Frq: 18.2; 24;
Matches 245; Conservative 0; Mismatches 51; Indels 13; Gaps 27
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11 136 GTTAATGCTGCTATATGAGCAAAATTTTGAAGCTGATGACGATGCAGATGCAGATC 247
29 148 GTCTTTAAAGTGAATGCTGCTATATGAGCAAAATTTTGAAGCTGATGACGATGCAGATC 177
29 146 GTCTTTAAAGTGAATGCTGCTATATGAGCAAAATTTTGAAGCTGATGACGATGCAGATC 1605
29 146 GTCTTTAAAGTGAATGCTGCTATATGAGCAAAATTTTGAAGCTGATGACGATGCAGATC 1665
DB 176 AATATCAAAATTTTGAAGCTGCTATATGAGCAAAATTTTGAAGCTGATGACGATGCAGATC 129
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DB 68 AGATTTCATCTTGTATATGAGCAAAATTTTGAAGCTGATGACGATGCAGATGCAGATC 10
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DB 7 AAAAAAAA 1
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